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Managing Livestock-Associated Zoonoses: Challenges, Surveillance, and Preventative Strategies within a One Health Framework

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Zoonotic diseases transmitted from livestock to humans present persistent global health and economic challenges. This review aims to provide a comprehensive analysis of major livestock-associated zoonoses, focusing on their causative agents, transmission pathways, clinical impacts, surveillance challenges, and strategies for control. Using a narrative literature review methodology, relevant peer-reviewed studies, epidemiological reports, and global health data were examined to synthesize current knowledge. The findings highlight key zoonotic pathogens such as *Brucella spp.*, *Mycobacterium bovis*, *Coxiella burnetii*, avian and swine influenza viruses, *Burkholderia pseudomallei*, and others, underscoring diverse transmission routes including foodborne, respiratory, vector-borne, and environmental exposure. Significant challenges persist in managing these diseases, particularly in low-resource settings, due to weak veterinary infrastructure, inconsistent surveillance, antimicrobial resistance, and the influence of climate change. However, emerging technologies such as genomic epidemiology, AI-based analytics, and participatory epidemiology offer promising tools for early detection and outbreak control. The review advocates for a coordinated One Health approach that integrates human, animal, and environmental health sectors. Strengthening surveillance, improving biosecurity, promoting public awareness, and fostering international collaboration are critical to mitigating zoonotic threats and building resilient global health systems.

Keywords: Biosecurity, economic impact of zoonoses, environmental transmission, global health security, integrated health systems, pathogens, surveillance.

INTRODUCTION

Zoonotic diseases are transmissible infections from animals to humans. Animals contribute significantly to the global disease burden as reservoirs (carriers that transmit the disease without showing symptoms) or intermediary hosts (organisms responsible for transferring the diseases between species). According to Diamond (2002), zoonotic infections have affected human health since agriculture and animal domestication over 10,000 years ago. Pathogen spillover is the transmission of a pathogen from its natural reservoir host to a new species, often humans, where it can cause disease. This spillover from close human-animal contact caused diseases that still harm humans today. Approximately 60% of human infectious diseases originate from animals, with 75% of emerging infections classified as zoonoses (Cleaveland *et al.*, 2001; Jones *et al.*, 2008). As amplifiers or bridges between wildlife and humans, livestock are crucial to zoonotic disease transmission. The 2009 swine-origin H1N1 influenza pandemic and the camel-associated MERS-CoV crisis demonstrate the persistent threat of livestock-associated zoonoses (Osztovits *et al.*, 2009). These epidemics have health and economic consequences, including trade restrictions, decreased production, and vast agricultural financial losses (Grace *et al.*, 2017). Developing countries have a greater rate of zoonotic infections due to close proximity between humans and livestock, poor biosecurity, and inadequate veterinary services (Jost *et al.*, 2021). Agricultural intensification, urbanization, and globalization have increased zoonotic disease threats. High animal numbers and extensive supply chains encourage disease spread across areas and populations in modern livestock production systems (Baker *et al.*, 2022). Zoonotic infections are spread by direct contact with infected animals, contaminated food and water, and environmental exposure. Transmission processes vary by pathogen and circumstance, such as *Coxiella burnetii* (which causes Q fever) is spread by inhaling polluted aerosols, while

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Salmonella is spread through the consumption of contaminated animal products. Certain occupations, like farming, slaughterhouse work and veterinary practice, pose a greater risk due to occasional exposure (Nadeem *et al.,* 2023). Antimicrobial resistance (AMR) limits treatment options and worsens infections, complicating zoonotic disease control. Overuse of antibiotics in livestock production systems selects resistant bacteria, endangering animal and human health (Rahman *et al.,* 2022). The One Health paradigm coordinates multidisciplinary efforts to address these concerns, integrating human, animal and environmental health. It is a collaborative approach that integrates human, animal, and environmental health to address complex health threats like zoonotic diseases and antimicrobial resistance. It emphasizes cross-sector coordination among health professionals, veterinarians, ecologists, and policymakers for holistic and sustainable solutions. This comprehensive review examines livestock-associated zoonotic diseases, their management issues, surveillance methods and prevention methods. This article assembles recent research and identifies knowledge gaps to inform zoonotic risk mitigation and public health policy.

Overview of major livestock associated zoonoses

***Q Fever (Coxiella burnetii)*:** Q fever is caused by *Coxiella burnetii*, an obligate intracellular bacterium (which needs a host to survive) with high environmental endurance. In 1937, *C. burnetii* was discovered by Derrick (1937) during a slaughterhouse fever outbreak in Brisbane, Australia. Its Gram-negative cell wall resists gram staining because of a thin peptidoglycan layer and outer membrane (Eldin *et al.,* 2017). Antigenic phase variation, driven by lipopolysaccharide (LPS) complexity, contributes to the pathogen's virulence and environmental persistence (Miller *et al.,* 2020; Pechstein *et al.,* 2018). Though domestic animals, marine mammals, birds, reptiles, and ticks are susceptible to *C. burnetii*, cattle, sheep, and goats are the main reservoirs. Infected animals lose the bacteria in delivery, milk, urine, and faeces. Limited person-to-person transmission occurs when people inhale contaminated aerosols from animal placentas, urine or feces (Eldin *et al.,* 2017; Pechstein *et al.,* 2018, España *et al.,* 2020). Raw dairy products, blood transfusions, sexual transmission and laboratory exposure are other routes (Kersh *et al.,* 2013; Signs *et al.,* 2012). Self-abortion, endometritis, mastitis and infertility may occur in infected animals (Eldin *et al.,* 2017). In humans, Q fever can cause acute febrile illness with pneumonia or hepatitis or a persistent condition with endocarditis occurring in people (Angelakis and Raoult, 2010). The incubation period shows a wide range of 7-32 days, with an average of 18 days (España *et al.,* 2020). Serology, PCR or microbial cultures help in diagnosis of Q fever (Pechstein *et al.,* 2018). Q fever is a global health issue as the US reported 212 instances, including 178 acute and 34 chronic infections whereas the EU reported 950 in 2019 (Boelaert *et al.,* 2021). Egypt has 16% seroprevalence, while Chad has 1% (Eldin *et al.,* 2017). From 2007 to 2010, the Netherlands had the greatest outbreak, with over 4,000 cases and likely over 40,000 infections (Eldin *et al.,* 2017). French Guiana has the greatest prevalence of *C. burnetii* with 24% of community-acquired pneumonia (Epelboin *et al.,* 2012). While animal vaccination and herd culling diminish transmission, the bacterium's environmental resistance makes eradication difficult (Roest *et al.,* 2011).

Important research gaps still exist despite tremendous advancements in our knowledge of Q fever and *C. burnetii*. The role of non-traditional reservoirs in the transmission dynamics and the bacterium's exceptional environmental resilience and survival are unknown. Underreporting due to irregular worldwide surveillance, insufficient understanding of chronic disease pathophysiology and the lack of a widely accessible human vaccination underline the need for targeted study.

***Brucellosis (Brucella spp.)*:** Brucellosis is a globally significant zoonotic disease caused by intracellular pathogens from the genus Brucella (Galinska *et al.,* 2013). These pathogens can multiply within phagocytic cells, with humans serving as end hosts (Franco *et al.,* 2007). Four species infect humans: B. abortus, B. canis, B. melitensis, and B. suis. Of these, B. melitensis is the most frequently obtained from ruminants, mainly sheep and goats, where it causes impaired fertility and abortions (Amjadi *et al.,* 2019; Głowacka *et al.,* 2018). *Brucella abortus* primarily affects cattle and poses a significant risk of zoonotic transmission to humans through various routes, including consumption of infected food and dairy products, occupational exposure, inhalation of aerosols, and direct contact with fetal fluids or contaminated materials (Rubach *et al.,* 2013; Amjadi *et al.,* 2019). Consequently, this makes veterinarians, farmers and abattoir workers vulnerable to infection. Secondary transmission can occur through mucous membrane contact, lactation, sexual intercourse and transfusion of infected blood or tissues (Tuon *et al.,* 2017). Although these routes have a minimal role in the disease burden comparatively, primary zoonotic transmission from infected animals. Human brucellosis manifests with diverse and often non-specific symptoms, including systemic presentations such as fever, chills, fatigue, and night sweats, as well as localized complications like epididymoorchitis, spondylodiscitis, neurobrucellosis, and endocarditis (Tuon *et al.,* 2017). Although brucellosis remains a significant zoonosis worldwide, it disproportionately impacts populations in developing countries due to inadequate animal health measures and high consumption of unpasteurized dairy products (Amjadi *et al.,* 2019; Rubach *et al.,* 2013). The disease is endemic in the Middle East, the Mediterranean rim, Asia, Africa, and South and Central America, with global human cases estimated to range between 500,000 and 12.5 million annually (Głowacka *et al.,* 2018; Hull and Schumaker, 2018). In sub-Saharan Africa, seroprevalence rates vary widely, from 24.1% in the region to 31.8% in Nigeria, 17% in

Uganda, and lower rates in Tanzania, Chad, and the Central African Republic (Awah-Ndukum *et al.,* 2018). The economic burden of brucellosis is immense, particularly in regions reliant on livestock production. Brucellosis imposes significant economic losses on the livestock sector. In Nigeria, the disease causes substantial losses to cattle producers due to stillbirths, reduced calving rates, infertility, along diminished productivity, amounting to approximately USD 224 million annually. Similar losses are reported in South Africa (USD 37.5 million) and the United States (USD 800 million) (Mai *et al.,* 2012).Rinderpest, a deadly cattle plague introduced to Sub-Saharan Africa in 1887, caused the death of over 90% of African-owned cattle, triggering massive famine and socio-economic collapse. Coordinated efforts led by the FAO and OIE included mass vaccination (notably with Plowright's TCRV vaccine), strict surveillance, and conflict-sensitive community engagement across East Africa. The last outbreak occurred in Kenya in 2001, and by 2011, all African countries were certified rinderpest-free, marking it as the first animal disease to be eradicated globally. This success underscores the importance of One Health collaboration and persistent multinational coordination in combating transboundary animal diseases (Jain, 2023). In 2023, Australia effectively managed a rare *Brucella melitensis* cluster through rapid genomic sequencing, coordinated public health actions, and inter-agency response, despite no identifiable source. The country remains officially free of *B. melitensis* in livestock, highlighting the strength of its surveillance, biosecurity, and outbreak management system (Metlapalli *et al.,* 2025).

In contrast, Brucellosis is rare in developed countries like the United States, where only 80–120 cases are reported annually (Centers for Disease Control and Prevention, 2021). Notably, Syria reports the highest global brucellosis prevalence, with 1603.4 cases per million individuals, followed by Mongolia (391), Iraq (268.8), Tajikistan (211.9), Saudi Arabia (149.5) and Iran (141.6) (Hull and Schumaker, 2018). In China, brucellosis remains a significant public health concern, with an incidence rate of 4.2 cases per 100,000 people reported in 2014 (Zheng *et al.,* 2018). Despite advancements in brucellosis control in developed countries, the persistently high incidence in endemic regions highlights the urgent need for strengthened surveillance, improved diagnostic tools, and accessible vaccination programs to mitigate its global impact.

***Tuberculosis (Mycobacterium bovis)*:** Zoonotic pathogens Mycobacterium caprae and Mycobacterium bovis cause tuberculosis (TB) in animals and humans. M. caprae causes few human TB cases and mostly affects goats, sheep, cattle, and other animals in Europe (Kozińska *et al.,* 2020; Prodinger *et al.,* 2014). M. bovis mostly infects cattle but can spread to other mammals including humans by aerosols, milk, meat, or direct contact (Kaneen *et al.,* 2010; Khan *et al.,* 2019). Zoonotic TB caused 140,000 cases in 2019, predominantly in Africa (50%) and South-East Asia (31%), but underreporting may increase the true number (WHO, 2021). Badgers, wild boars, and buffalo are reservoirs, making livestock disease control difficult (Palmer, 2013; De lisle *et al.,* 2002). In underdeveloped countries, poor hygiene, lack of animal product control and co-infections like HIV/AIDS enhance the likelihood of M. bovis transmission (O'Reilly and Dabron, 1995; Michel *et al.,* 2010; El-Syed *et al.,* 2016). Milk pasteurization, testing and culling have reduced cases in developed countries.

***Salmonellosis (Salmonella spp.)*:** Salmonella is a Gram-negative, rod-shaped, facultative anaerobic Entero-bacteriaceae bacterium that causes widespread zoonotic diseases (Jajere, 2019). Two primary species are *S. bongori* and *S. enterica*, with around 2600 serovars. Invasion and intracellular replication are the main virulence factors of S. enterica serovars Enteritidis and Typhimurium, which cause most human infections (Jajere, 2019; WHO, 2021). Food (e.g., eggs, milk, meat, vegetables), water, direct contact with infected animals or feces and the farm-to-fork pathway cause the continuous spread of disease (WHO, 2021). Pests like flies, rodents and beetles are important vectors in poultry and cattle production (Jajere, 2019). Diarrhea, stomach discomfort, fever, and vomiting are common symptoms of salmonellosis. EU reported 87,923 cases in 2019, while US Salmonella causes 1.35 million illnesses and 420 fatalities annually, largely from contaminated food (Boelaert *et al.,* 2021). Non-typhoidal salmonellosis is most prevalent in Sub-Saharan Africa, mainly because of poor food safety regulations, unsanitary conditions and extensive contamination of poultry products. Control methods for contamination are good agricultural practices, hazard analysis and critical control points (a food safety management system that detects and lowers hazards in the production process), vaccination and proper cooking, but the use of antibiotics is limited due to resistance. Effective regional control strategies require thorough surveillance, consisting of microbial analysis of food products, disease incidence tracking and routine testing in poultry farms and processing plants to assess contamination early (WHO, 2021).

***Other pathogen*:** Zoonotic infections persist as a serious hazard to human and animal health. These diseases fall under the category of their mode of transmission: foodborne infections (listeriosis), respiratory infections (swine influenza, avian influenza), vector-borne infections (West Nile fever) and environmental infections (anthrax, legionellosis and melioidosis). Avian influenza viruses (AIVs), mostly H5 and H7 subtypes, infect poultry and wild birds, causing human infections through direct contact or product intake. In H5N1 and H7N9 outbreaks, minor respiratory disease can lead to severe pneumonia and multi-organ failure (Zhou *et al.,* 2018; Li *et al.,* 2021; WHO, 2021). Influenza A viruses are transmitted by respiratory secretions, posing a zoonotic danger, especially for swine workers, with reassortant strains like H1N1pdm09 causing pandemics

Table 1. Overview of major zoonotic diseases associated with livestock.

Disease	Causative Agent	Key Symptoms in Humans	Modes of Transmission	Epidemological insights	Endemic Regions	Effective Control Strategies	References
Q fever	*Coxiella burnetii*	Fever, pneumonia, liver inflammation, and heart infection	Breathing in airborne particles, consuming contaminated food, blood transfusion, or sexual contact	Reported cases: EU—950 (2019), USA—178 (2019)	EU, Australia, USA	Q-Vax® is a phase I whole-cell vaccine, and its licensed use is limited to Australia	Boelaert *et al.*, 2021; Eldin *et al.*, 2017; (Long, 2021)
Brucellosis	*Brucella abortus, B. melitensis, B. canis, B. suis*	Fever, chills, fatigue, joint pain, neuroinflammation, and heart valve infection	Ingestion of infected dairy or meat, occupational exposure, or airborne transmission	Global: ~500,000 cases/year; EU—310 (2019), USA—80–120 cases/year	EU, USA, Turkey	Livestock vaccination (*S19, RB51*), test-and-slaughter policies, pasteurization, public education	Boelaert *et al.*, 2021; Amjadi *et al.*, 2019, (ÇAKIR and YENİ, 2025)
Tuberculosis	*Mycobacterium bovis, M. caprae*	Fatigue, fever, respiratory symptoms, and complications in bones, joints, or the nervous system	Airborne spread, consumption of unpasteurized dairy, or infected meat	EU—147 cases (2019), USA—7174 cases (2020)	African regions, EU, USA	Tuberculin testing, culling, milk pasteurization, wildlife management (badgers/deer)	Boelaert *et al.*, 2021; Kozi´ nska *et al.*, 2020; (Wilson, 2020); (IRAGENA *et al.*, 2025)
Trichinellosis	*Trichinella sp.*	Gastrointestinal distress, muscle pain, heart inflammation, facial swelling, and neurological issues	Eating undercooked or raw meat containing larvae	EU—96 cases (2019), USA—90 cases (2008–2012)	Argentina, EU, USA	Meat inspection, freezing/cooking regulations, consumer education. YOLOv5 is an image recognition tool easily trained to count muscular first stage larvae (L1) and recognize morphological differences.	(Sánchez-Montejo *et al.*, 2025); Fariña *et al.*, 2025)
Yersiniosis	*Yersinia enterocolitica, Y. pseudotuberculosis*	Abdominal pain, fever, nausea, vomiting, and diarrhea	Consumption of undercooked pork, contaminated dairy, seafood, vegetables, or water	EU—6961 cases annually; USA—~117,000 cases/year	East Asia, EU, USA	Pork processing controls, hygiene, water treatment, cold chain enforcement	Boelaert *et al.*, 2021; Laukkanen-Ninios *et al.*, 2014
Salmonellosis	*Salmonella sp.*	Diarrhea, abdominal cramps, fever, nausea, and vomiting	Eating contaminated foods (e.g., eggs, meat, milk), drinking unclean water, direct contact with infected animals	EU—87,923 cases (2019), USA—~1.35 million cases/year; Sub-Saharan Africa—535,500 cases (2019)		Food safety enforcement : Hazard Analysis Critical Control Point (HACCP), poultry vaccination, hygiene education	Boelaert *et al.*, 2021; (Betiku *et al.*, 2025)

(Smith *et al.*, 2009; Chastagner *et al.*, 2019). Food and water contamination spreads Listeria monocytogenes-caused listeriosis. Pregnant women and immunocompromised people are at risk of meningitis and sepsis (Buchanan, *et al.*, 2017). Glanders, caused by Burkholderia mallei, causes inflammatory lesions and systemic disease in solipeds and humans. However, Glanders remains in Asia, Africa, and South America with the ability to re-emerge because of the expanding international trade and dissemination through animal trade or contaminated equipment (Khan *et al.*, 2013). The mosquitoes that carry West Nile Virus (WNV) from infected birds spread neuroinvasive illness in people and animals. To curb WNV, surveillance through tracking of mosquito population and avian carrier detection is necessary. Similarly, to prevent outbreaks of avian influenza, systematic serological monitoring in poultry farms and live bird markets is pivotal (Hadfield *et al.*, 2019). In tropical places, *Burkholderia pseudomallei* causes melioidosis, which affects humans and animals through soil or water contact. It is called the "Great Mimicker" for its high mortality and varied symptoms (Chakravorty and Heath, 2019; Le Tohic *et al.*, 2019)

Better biosecurity, vaccination, surveillance, and public knowledge can control these infections. One Health coordination is needed to reduce zoonotic threats and preserve public health (Buchanan *et al.*, 2017; Le Tohic *et al.*, 2019).

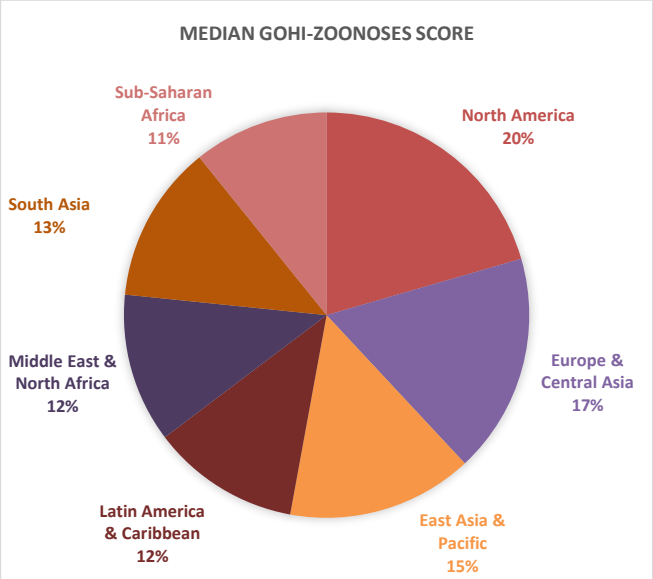
MEDIAN GOHI-ZOONOSES SCORE
Sub-Saharan Africa 11%
North America 20%
South Asia 13%
Middle East & North Africa 12%
Europe & Central Asia 17%
Latin America & Caribbean 12%
East Asia & Pacific 15%

Figure 2. Global One Health Index (GOHI) Zoonoses score of different regions (Sun *et al.*, 2024).

***Transmission mechanism*:** Zoonotic diseases are transmitted to humans through multiple mechanisms depending on the pathogen involved as presented in figure 3. Direct contact with infected animals or their secretions is a common route for diseases like brucellosis, which spreads through occupational exposure in farming and slaughterhouse environments (Boelaert *et al.,* 2021; Amjadi *et al.,* 2019). Inhalation of airborne particles plays a major role in Q fever transmission, caused by *Coxiella burnetii*, particularly in areas with contaminated dust from livestock environments (Eldin *et al.,* 2017; Boelaert *et al.,* 2021). Foodborne pathways are significant for diseases like trichinellosis, which results from consuming undercooked meat containing *Trichinella* larvae, and salmonellosis, spread by contaminated animal products like meat, eggs, and milk (Bilska-Zajac *et al.,* 2021; Boelaert *et al.,* 2021). Consumption of unpasteurized dairy or infected meat can also cause zoonotic tuberculosis from *Mycobacterium bovis* (Kozińska *et al.,* 2020). Waterborne transmission and poor sanitation contribute to yersiniosis, often linked to contaminated pork or untreated water (Laukkanen-Ninios *et al.,* 2014). Airborne and respiratory droplets are responsible for the spread of swine influenza, especially through contact with infected pigs (Smith *et al.,* 2009; Myers *et al.,* 2006). These transmission modes highlight the complexity of zoonotic disease ecology and the need for integrated surveillance across food, environment, and animal sectors (Boelaert *et al.,* 2021).

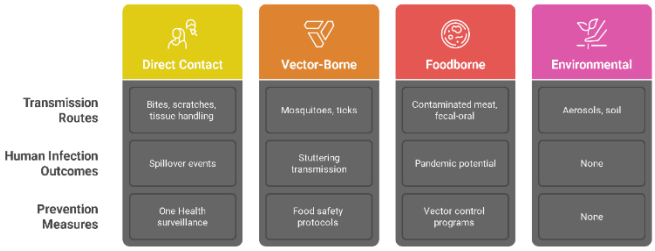

Figure 3. Zoonoses Disease Transmission Chains.

Complex problems make livestock-associated zoonotic diseases difficult to handle. The complexity of transmission channels is a major issue. Zoonotic infections can spread by direct contact with diseased animals, contaminated items, environmental reservoirs, or vector-borne pathways (Grace *et al.,* 2012). *Coxiella burnetii* persists in the environment, making eradication difficult (Maurin and Raoult, 1999). Moreover, economic as well as community level constraints hinder the management of zoonotic diseases, resulting in elevated disease burden, restricted trades and financial losses in affected areas. Zoonotic epidemics cost animal slaughter, production loss, trade restrictions and public health (Grace *et al.,* 2012). Developing countries face challenges in the management of livestock-associated zoonotic diseases due to weak veterinary infrastructure, biosecurity and zoonotic awareness (Torgerson and Macpherson, 2011). Transmission complexity, weak veterinary infrastructure, antimicrobial resistance and climate changes contribute to long-lasting illness effects and spread. More problems arise from antibiotic resistance. Strain resistance from antibiotic overuse and misuse in animal agriculture makes standard therapies ineffective, which complicates zoonotic disease treatment in livestock and also increases the chances of resistant infections in humans (Van Boeckel *et al.,* 2015). Antimicrobial resistance (AMR) complicates zoonotic disease management and increases animal and human treatment failures (Holmes *et al.,* 2016). Climate change influences zoonotic disease dynamics through shifts in vector populations (e.g., facilitating mosquito population spread due to rising temperatures) and influencing pathogen persistence in environmental reservoirs. Additionally, increased international trade spreads zoonotic pathogens across the borders (Jones *et al.,* 2008). For effective zoonotic disease control approaches like the coordinated One Health approach, coordinating efforts at local, national and global levels is indispensable for the prevention of zoonotic outbreaks. Strengthening surveillance systems, regulating antibiotic usage policies and upgrading veterinary service networks may help to mitigate these interrelated issues.

Surveillance and Biosecurity Strategies

***Surveillance strategies*:** Detecting, preventing, and controlling zoonotic disease epidemics requires surveillance. Zoonotic disease surveillance uses active and passive systems, molecular diagnostics, and genomic epidemiology. Active surveillance targets high-risk people and places like wet markets and abattoirs, livestock workers and densely populated animal farms. In contrast, passive surveillance relies on diagnosed cases reported in healthcare and veterinary systems (Häsler *et al.,* 2014). Surveillance has a key role in tracing, and mitigating the zoonotic disease outbreaks. Active and passive surveillance systems, together with cutting-edge molecular diagnostics and genomic analysis, form the essential framework for outbreak monitoring. However, these approaches encounter obstacles including data underreporting, lack of standardized diagnostics and limited data exchange systems. Progressive measures, such as inclusive epidemiological approaches, tech-driven solutions like Artificial intelligence and Geographic Information System and One Health collaborations, provide strategies to enhance global zoonotic disease surveillance. Despite these developments, global zoonotic disease surveillance is limited. Case underreporting, especially in resource-constrained settings, impairs disease trend tracking. Diagnostic standards vary across and within nations, causing reporting discrepancies (Grace *et al.,* 2012). Bad infrastructure and data-sharing protocols restrict surveillance. Zoonotic disease databases are scarce in low- and middle-income countries, making epidemic response coordination challenging. Improving surveillance deficiencies demands novel strategies. One such strategy is

participatory epidemiology, which helps cover gaps, by involving local communities in disease monitoring. Involving local residents and applying indigenous knowledge can assist discover abnormal cattle sickness and mortality trends (Zinsstag *et al.,* 2011). It builds trust and empowers communities to prevent.

Technological advances have altered surveillance. Next-generation sequencing (NGS) efficiently discovers zoonotic illnesses and their genetic variations, revealing disease origins and transmission routes. AI and machine learning-powered real-time data analytics can find outbreak abnormalities in vast databases. GIS is mapping illness hotspots and predicting zoonotic pathogen distribution to better resource allocation and targeted interventions (Pigott *et al.,* 2014). Solving surveillance issues requires cross-sector and international cooperation. Integrating human, animal, and environmental health systems in the One Health paradigm helps fill surveillance gaps. Regional and worldwide networks like the Global Early Warning System (GLEWS) increase zoonotic preparation and information exchange (FAO, 2010).

***Surveillance Challenges*:** Different practical and systemic errors reduce the effectiveness of surveillance, especially in middle and low-income countries. These challenges are:

Remote areas in kenya lack PCR machines and refrigeration facilities for sample storage, causing delays in disease confirmation for pathogens such as Brucella spp. And Coxiella burnetii. Secondly lack of transportation facilities leads to hindrance in the shipment of biological samples to central laboratories. Effective zoonotic disease surveillance under One Health frameworks faces substantial implementation challenges, as demonstrated by multiple studies. In Australia, surveillance systems are hampered by poor inter-sectoral communication and siloed approaches, compounded by unclear definitions and lack of political commitment (Johnson *et al.,* 2018). Similar barriers emerge in Western Kenya, where collaborative zoonotic disease surveillance for threats like rabies and anthrax is undermined by inadequate resource allocation and absence of formal operational frameworks, despite some successful cross-sectoral cooperation (Meidenbauer, 2017). Surveillance gaps are particularly acute in animal health systems, as shown in Uganda's West Nile region where animal disease surveillance integration scores just 0.20 for data collection/analysis compared to 0.92 for human systems, with critical limitations in laboratory capacity and real-time reporting (Behumbiize, 2019). These challenges are further exemplified by the National Capital Region experience, where 70% of veterinarians report limited surveillance system access and fewer than 50% notify authorities about zoonotic diseases (Meidenbauer, 2017). Even in advanced systems like Denmark's, integration is hindered by legal barriers to data sharing between animal and human health sectors and unclear ministerial responsibilities (Houe *et al.,* 2019). These systemic barriers - including laboratory shortages, data fragmentation, resource constraints, and weak governance structures - collectively undermine timely detection and response to emerging zoonotic threats across diverse geographical and economic contexts.

Table 2. Future direction and recommendations.

Future Directions	Recommendations
Strengthen global One Health initiatives	Promote cross-sectoral collaborations between human, animal, and environmental health systems.
Advance molecular and genomic surveillance	Invest in next-generation sequencing technologies for early pathogen detection and characterization.
Expand participatory epidemiology	Engage local communities in surveillance and prevention efforts.
Improve biosecurity measures	Implement strict hygiene protocols and regular health monitoring in livestock farms and markets.
Address antimicrobial resistance	Enforce regulations on antibiotic use in livestock and promote alternatives like probiotics.
Enhance education and public awareness	Develop targeted educational campaigns for farmers, veterinarians, and the public.
Leverage artificial intelligence and GIS	Utilize AI-driven analytics and GIS for real-time monitoring and prediction of zoonotic outbreaks.
Support vaccination programs	Scale up vaccination of livestock against key zoonotic pathogens in high-risk regions.
Foster international collaboration	Strengthen data-sharing frameworks and global networks like GLEWS for coordinated responses.
Monitor climate change impacts	Study and address the influence of changing climates on zoonotic pathogen distribution.
Integrate socioeconomic considerations	Incorporate economic impact assessments and livelihood concerns into zoonosis control strategies.
Strengthen veterinary public health systems	Improve infrastructure, staffing, and training in veterinary services, especially in low-resource areas.
Promote sustainable livestock systems	Encourage practices that reduce environmental degradation and minimize disease spillover risks.
Facilitate rapid outbreak response units	Establish mobile teams for immediate investigation and containment of zoonotic outbreaks.
Standardize data collection and reporting	Develop interoperable platforms and standardized indicators for zoonotic disease surveillance.

***Research Gap*:** This review identifies key gaps in research needed to advance livestock-associated zoonotic disease management. However, the underreporting remains a global problem, especially in low- and middle-income countries, where a weak laboratory infrastructure, weak surveillance systems, and weak data integration are barriers to timely detection. For pathogens such as Coxiella burnetii and Brucella spp., the environmental stability and transmission dynamics commercially produced from the non-traditional

reservoirs are not well understood even till now. The absence of standard diagnostic assays and harmonised reporting protocols between sectors and countries complicates the tracking of infectious animal diseases.

While some endemic and emerging regions lack zoonotic disease burden data, this problem is particularly acute for neglected diseases (like melioidosis and glanders). Existing policy interventions have seldom been reviewed for their effectiveness against zoonoses and their socioeconomic impacts have been poorly described. Furthermore, these community-centred approaches and participatory epidemiology approaches are promising, but further work is needed to determine how to formally integrate these in surveillance systems. Low coverage, gaps in the cold chain logistics of vaccines, and their reduced efficacy in different ecological settings also restrict the controllability. Filling these gaps will require interdisciplinary research and context-tailored approaches within a One Health framework.

***Conclusion*:** Zoonotic diseases, especially livestock associated ones, e.g., brucellosis, Q fever and tuberculosis, remain a significant global public health and economic burden. The major obstacles that impede effective management are disintegrated surveillance systems, absence of early detection mechanisms, poor biosecurity practices and the rising danger of antimicrobial resistance. Nowhere are these challenges compounded more than in low-resource settings and areas of convergence between humans, domestic animals, and wildlife, as environmental change continues to exacerbate increased exposure to human–animal interactions and inadequate cross-sectoral coordination between public and animal health sectors.

The One Health approach is central to overcoming these challenges. By promoting integrated collaboration across human, animal, and environmental health domains, One Health strengthens surveillance, enhances outbreak preparedness, and supports more holistic responses to zoonotic threats. Its value is evidenced by successes such as the global eradication of rinderpest and the effective control of *Brucella melitensis* in Australia—demonstrating that multisectoral coordination can lead to sustainable disease control.

Policy recommendations should focus on strengthening veterinary public health systems, institutionalizing cross-sector data sharing platforms, supporting livestock vaccination and biosecurity enforcement, and embedding One Health education in both health and agricultural sectors. Governments and international bodies must also invest in capacity building for laboratory diagnostics, mobile outbreak response teams, and real-time disease monitoring systems.

In terms of further research, priority areas include understanding zoonotic disease dynamics in high-risk ecosystems, evaluating long-term impacts of control programs, and developing context-specific tools for community-based surveillance and behavior change. Moreover, innovation in predictive modeling, climate-linked risk mapping, and digital health integration will be essential for building resilient and proactive zoonotic disease response systems.

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Consent to participate N/A

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REFERENCES

Amjadi, O., A. Rafiei, M. Mardani, P. Zafari and A. Zarifian. 2019. A review of the immunopathogenesis of brucellosis. Infectious Diseases 51:321-333.

Angelakis, E. and D. Raoult. 2010. Q fever. Veterinary microbiology 140:297-309.

Awah-Ndukum, J., M.M.M. Mouiche, L. Kouonmo-Ngnoyum, H.N. Bayang, T.K. Manchang, R.S.N. Poueme, J. Kouamo, V. Ngu-Ngwa, E. Assana, K.J.M. Feussom and A.P. Zoli. 2018. Seroprevalence and risk factors of brucellosis among slaughtered indigenous cattle, abattoir personnel and pregnant women in Ngaoundéré, Cameroon. BMC infectious diseases 18:1-13.

Baker, R.E., A.S. Mahmud, I.F. Miller, M. Rajeev, F. Rasambainarivo, B.L. Rice and C.J.E. Metcalf. 2022. Infectious disease in an era of global change. Nature Reviews Microbiology 20:193-205.

Behumbiize, P., J. Lule and B. Magoba. 2019. Evaluation of the implementation and utilisation of a case based diseases surveillance (electronic Integrated Disease Surveillance and Reporting (eIDSR-CBS)) in the West Nile region: August 2018 to February 2019. Texila Int J Pub Health 7:34-48.

Betiku, E., T.T. Ogundipe, T. Kalapala and T. Obe. 2025. A Mini-Review on Multi-Hurdle Control of Salmonella Along Poultry Production Continuum. Animals 15:875.

Bilska-Zając, E., M. Różycki, W. Korpysa-Dzirba, A. Bełcik, A. Ziętek-Barszcz, M. Włodarczyk-Ramus, A. Gontarczyk and T. Cencek. 2021. Trichinella outbreaks on pig farms in Poland in 2012–2020. Pathogens 10:1504.

Boelaert, F., A. Stoicescu, G. Amore, W. Messens, M. Hempen, V. Rizzi, S.E. Antoniou, F. Baldinelli, E. Dorbek-Kolin, Y. Van der Stede and T. Niskanen. 2021. The European Union One Health 2019 Zoonoses Report. EFSA Journal vol. 19.

Buchanan, R.L., L.G. Gorris, M.M. Hayman, T.C. Jackson and R.C. Whiting. 2017. A review of Listeria monocytogenes: An update on outbreaks, virulence, dose-response, ecology, and risk assessments. Food Control 75:1-13.

ÇAKIR, Ş. and D.K. YENİ. 2025. The Example of Çankırı Province in Combating Brucellosis in Cattle. RESEARCH & PRACTICE in VETERINARY & ANIMAL SCIENCE:11.

Centers for Disease Control and Prevention (CDCP). 2021. U.S. One Health Zoonotic Disease Prioritization Report. Available online at: https://www.cdc.gov/onehealth/pdfs/us-ohzdpreport-508.pdf (Accessed 25 November 2021).

Chakravorty, A. and C.H. Heath. 2019. Melioidosis: an updated review. Australian Journal of General Practice 48:327-332.

Chastagner, A., V. Enouf, D. Peroz, S. Hervé, P. Lucas, S. Quéguiner and G. Simon. 2019. Bidirectional human–swine transmission of seasonal influenza A (H1N1) pdm09 virus in pig herd, France, 2018. Emerging infectious diseases 25:1940.

Cleaveland, S., M.K. Laurenson and L.H. Taylor. 2001. Diseases of humans and their domestic mammals: Pathogen characteristics, host range, and the risk of emergence. Philosophical Transactions of the Royal Society B: Biological Sciences 356:991-999.

De Lisle, G.W., R.G. Bengis, S.M. Schmitt and D.J.O. Brien. 2002. Tuberculosis in free-ranging wildlife: detection, diagnosis and management. Revue Scientifique et Technique-Office International des Epizooties 21:317-334.

Derrick, E.H. 1937. "Q" Fever, a new fever entity: Clinical features, diagnosis and laboratory investigation. Medical Journal of Australia 2:281-299.

Diamond, J. 2002. Evolution, consequences, and future of plant and animal domestication. Nature 418:700-707.

Eldin, C., C. Mélenotte, O. Mediannikov, E. Ghigo, M. Million, S. Edouard, J.L. Mege, M. Maurin and D. Raoult. D., 2017. From Q fever to *Coxiella burnetii* infection: a paradigm change. Clinical microbiology reviews 30:115-190.

El-Sayed, A., S. El-Shannat, M. Kamel, M.A. Castañeda-Vazquez and H. Castañeda-Vazquez. 2016. Molecular epidemiology of *Mycobacterium bovis* in humans and cattle. Zoonoses and Public Health 63:251-264.

Epelboin, L., C. Chesnais, C. Boullé, A.S. Drogoul, D. Raoult, F. Djossou and A. Mahamat. 2012. Q fever pneumonia in French Guiana: prevalence, risk factors, and prognostic score. Clinical infectious diseases 55:67-74.

España, P.P., A. Uranga, C. Cillóniz and A. Torres. 2020. Q fever (*Coxiella burnetii*). Seminars in Respiratory and Critical Care Medicine 41:509-521.

FAO, OIE and WHO. 2010. The FAO-OIE-WHO collaboration: sharing responsibilities and coordinating global activities to address health risks at the animal-human-ecosystems interface. International Ministerial Conference on Animal and Pandemic Influenza, Hanoi, Vietnam.

Fariña, F.A., M.I. Pasqualetti, M. Winter, S. Abate, G. Daneri, A. Harrington, T. Aronowicz, C. Calvo, C. Lapuyade and F.A. D'Francisco. 2025. Assessment of Trichinella Infection in Animals from Argentina. Parasitologia 5:21.

Franco, M.P., M. Mulder, R.H. Gilman, and H.L. Smits. 2007. Human brucellosis. The Lancet Infectious Diseases 7:775-786.

Galinska, E.M. and J. Zagórski. 2013. Brucellosis in humans-etiology, diagnostics, clinical forms. Annals of agricultural and environmental medicine 20:233-238.

Głowacka, P., D. Żakowska, K. Naylor, M. Niemcewicz and A. Bielawska-Drozd. 2018. Virulence factors, pathogenesis and treatment. Polish journal of microbiology 67:151-161.

Grace, D., J. Gilbert, T. Randolph, E. Kang'ethe. 2012. The multiple burdens of zoonotic disease and an eco-health approach to their assessment. Tropical Animal Health and Production 44:67-73.

Grace, D., J. Lindahl, F. Wanyoike, B. Bett, T. Randolph and K.M. Rich. 2017. Poor livestock keepers: Ecosystem-poverty-health interactions. Philosophical Transactions of the Royal Society B: Biological Sciences 372:20160166.

Hadfield, J., A.F. Brito, D.M. Swetnam, C.B. Vogels, R.E. Tokarz, K.G. Andersen, R.C. Smith, T. Bedford and N.D. Grubaugh. 2019. Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. PLoS Pathogens 15:1008042.

Häsler, B., K.S. Howe, K.D.C. Stärk. 2014. Conceptualizing the technical relationship of animal disease surveillance to intervention and mitigation as a basis for economic analysis. BMC Veterinary Research. 10:171.

Holmes, A.H., L.S. Moore, A. Sundsfjord, M. Steinbakk, S. Regmi, A. Karkey, P.J. Guerin and L.J. Piddock. 2016.

Understanding the mechanisms and drivers of antimicrobial resistance. The Lancet:176-187.

Houe, H., S.S. Nielsen, L.R. Nielsen, S. Ethelberg and K. Mølbak. 2019. Opportunities for improved disease surveillance and control by use of integrated data on animal and human health. Frontiers in Veterinary Science 6:301.

Hull, N.C. and B.A. Schumaker. 2018. Comparisons of brucellosis between human and veterinary medicine. Infection ecology & epidemiology 8:1500846.

IRAGENA, J.d.D., E. Uwimaana, D. Semugenze, K. Komakech, A. Katamba, A. Martin, M. Joloba and W. Ssengooba. 2025. Uptake and rollout of the World Health Organization-endorsed technologies for Tuberculosis diagnosis in Africa: A systematic review of international evidence 2007-2021. medRxiv:2025.2002. 2006.25321799.

Ito, T., J.N.S. Couceiro, S. Kelm, L.G. Baum, S. Krauss, M.R. Castrucci and Y. Kawaoka. 1998. Molecular basis for the generation in pigs of influenza A virus with pandemic potential. Journal of Virology 72:7367-7373.

Jain, N.R. 2023. The First Animal Disease to be Eradicated in the History of Pandemic-Rinderpest. mLAC Journal for Arts, Commerce and Sciences (m-JACS) ISSN: 2584-1920 1:2-8.

Jajere, S.M. 2019. A review of Salmonella enterica with particular focus on the pathogenicity and virulence factors, host specificity and antimicrobial resistance including multidrug resistance. Veterinary World 12:504.

Johnson, I., A. Hansen and P. Bi. 2018. The challenges of implementing an integrated One Health surveillance system in Australia. Zoonoses and public health 65:e229-e236.

Jones, K.E., N.G. Patel, M.A. Levy, A. Storeygard, D. Balk, J.L. Gittleman and P. Daszak. 2008. Global trends in emerging infectious diseases. Nature 451:990-993.

Jost, C.C., C. Machalaba, W.B., Karesh, J.J. McDermott, D. Beltrán-Alcrudo, B. Bett and D.U. Pfeiffer. 2021. Epidemic disease risks and implications for veterinary services. Revue Scientifique et Technique 40:497-509.

Kaneene, J.B., R. Miller, I.N. De Kantor and C.O. Thoen. 2010. Tuberculosis in wild animals. The International journal of tuberculosis and lung disease 14:1508-1512.

Kersh, G.J., R. Priestley and R.F. Massung. 2013. Stability of *Coxiella burnetii* in stored human blood. Transfusion 53:1493-1496.

Khan, I., L.H. Wieler, F. Melzer, M.C. Elschner, G. Muhammad, S. Ali and M. Saqib. 2013. Glanders in animals: a review on epidemiology, clinical presentation, diagnosis and countermeasures. Transboundary and Emerging Diseases 60:204-221.

Khan, M.K., M.N. Islam, J. Ferdous and M.M. Alam. 2019. An overview on the epidemiology of tuberculosis. Mymensingh Medical Journal 28:259-266.

Kozińska, M., M. Krajewska-Wędzina, E. Augustynowicz-Kopeć. 2020. Mycobacterium caprae—the first case of the human infection in Poland. Annals of Agricultural and Environmental Medicine 27:151-153.

Laukkanen-Ninios, R., M. Fredriksson-Ahomaa, R. Maijala and H. Korkeala. 2014. High prevalence of pathogenic Yersinia enterocolitica in pig cheeks. Food microbiology 43:50-52.

Le Tohic, S., M. Montana, L. Koch, C. Curti and P. Vanelle. 2019. A review of melioidosis cases imported into Europe. European Journal of Clinical Microbiology & Infectious Diseases 38:1395-1408.

Li, S., Y. He, D.A. Mann and X. Deng. 2021. Global spread of Salmonella Enteritidis via centralized sourcing and international trade of poultry breeding stocks. Nature Communications 12:1-12.

Long, C.M. 2021. Q fever vaccine development: current strategies and future considerations. Pathogens 10:1223.

Mai, H.M., P.C. Irons, J. Kabir and P.N. Thompson. 2012. A large seroprevalence survey of brucellosis in cattle herds under diverse production systems in northern Nigeria. BMC Veterinary Research 8:1-14.

Maurin, M., D. Raoult. 1999. Q fever. Clinical Microbiology Reviews 12:518-553.

Meidenbauer, K.L. 2017. Animal surveillance: use of animal health data to improve global disease surveillance. Online journal of public health informatics 9:e147.

Metlapalli, M., F. Clarke, A.B. Pierce, N.L. Sherry, J.A. Lacey, E. Jalil, A. Tai, C. McGrath, T. Korman and J.H. McMahon. 2025. A cluster of Brucella melitensis in Melbourne, Australia 2023: clinical and public health actions. Communicable diseases intelligence (2018) 49

Michel, A.L., B. Müller and P.D. Van Helden. 2010. Mycobacterium bovis at the animal–human interface: A problem, or not. Veterinary Microbiology 140:371-381.

Miller, H.K., R.A. Priestley and G.J. Kersh. 2020. Transmission of *Coxiella burnetii* by ingestion in mice. Epidemiology and Infection 148:21.

Myers, K.P., C.W. Olsen, S.F. Setterquist, A.W. Capuano, K.J. Donham, E.L. Thacker and G.C. Gray. 2006. Are swine workers in the United States at increased risk of infection with zoonotic influenza virus? Clinical infectious diseases 42:14-20.

Nadeem, A., T. Nasrullah, A. Nasir, M.W. Nazar, A. Hussain, M.U. Iqbal, A. Rehman. 2023. Zoonosis in the food chain. Zoonosis. Unique Scientific Publishers, Faisalabad, Pakistan 1:361-373.

O'Reilly, L.M. and C.J. Daborn. 1995. The epidemiology of *Mycobacterium bovis* infections in animals and man: a review. Tubercle and Lung disease 76:1-46.

Osztovits, J., C. Balázs and J. Fehér. 2009. H1N1 influenza–pandemic, 2009. Orvosi Hetilap 150:2265-2273.

Palmer, M.V. 2013. Mycobacterium bovis: characteristics of wildlife reservoir hosts. Transboundary and Emerging Diseases 60:1-13.

Pechstein, J., J. Schulze-Luehrmann and A. Lührmann. 2018. *Coxiella burnetii* as a useful tool to investigate bacteria-friendly host cell compartments. International Journal of Medical Microbiology 308:77-83.

Pigott, D.M., N. Golding, A. Mylne, Z. Huang, A.J. Henry, D.J. Weiss, O.J. Brady, M.U. Kraemer, D.L. Smith, C.L. Moyes and S. Bhatt. 2014. Mapping the zoonotic niche of Ebola virus disease in Africa. eLife 3:e04395.

Prodinger, W.M., A. Indra, O.K. Koksalan, Z. Kilicaslan and E. Richter. 2014. Mycobacterium caprae infection in humans. Expert review of anti-infective therapy 12:1501-1513.

Rahman, M.M., M.A. Alam Tumpa, M. Zehravi, M.T. Sarker, M.D. Yamin, M.R. Islam and S. Cavalu 2022. An overview of antimicrobial stewardship optimization: the use of antibiotics in humans and animals to prevent resistance. Antibiotics 11:667.

Roest, H.I.J., J.J.H.C. Tilburg, W. Van der Hoek, P. Vellema, F.G. Van Zijderveld, C.H.W. Klaassen and D. Raoult. 2011. The Q fever epidemic in The Netherlands: history, onset, response and reflection. Epidemiology & Infection 139:1-12.

Rubach, M.P., J.E. Halliday, S. Cleaveland and J.A. Crump. 2013. Brucellosis in low-income and middle-income countries. Current opinion in infectious diseases 26:404-412.

Sánchez-Montejo, J., M. Marín, M.A. Villamizar-Monsalve, M.d.C. Vieira, B. Vicente, R. Peláez, J. López-Abán and A. Muro. 2025. AxiWorm: a new tool using YOLOv5 to test antiparasitic drugs against Trichinella spiralis. Parasites & Vectors 18:36.

Signs, K.A., M.G. Stobierski and T.N. Gandhi. 2012. Q fever cluster among raw milk drinkers in Michigan, 2011. Clinical infectious diseases 55:1387-1389.

Smith, G.J., D. Vijaykrishna, J. Bahl, S.J. Lycett, M. Worobey, O.G. Pybus, S.K. Ma, C.L. Cheung, J. Raghwani, S. Bhatt and J.M. Peiris. 2009. Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. Nature 459:122-1125.

Sun, Z.-S., E.-Y. Wan, Y.L. Agbana, H.-Q. Zhao, J.-X. Yin, T.-G. Jiang, Q. Li, S.-W. Fei, L.B. Wu and X.-C. Li. 2024. Global One Health index for zoonoses: A performance assessment in 160 countries and territories. Iscience 27

Taylor, L.H., S.M. Latham and M.E.J. Woolhouse. 2001. Risk factors for human disease emergence. Philosophical Transactions of the Royal Society B: Biological Sciences 356:983-989.

Torgerson, P.R., C.N.L. Macpherson. 2011. The socioeconomic burden of parasitic zoonoses: Global trends. Veterinary Parasitology. 182:79-95.

Tuon, F.F., R.B. Gondolfo and N. Cerchiari. 2017. Human-to-human transmission of *Brucella*—A systematic review. Tropical Medicine & International Health 22:539–546.

Upton, M. 2007. Scale and structures of the poultry sector and factors inducing change: Intercountry differences and expected trends. In Proceedings of the FAO Conference, November 2007:49-79.

Van Boeckel, T.P., C. Brower, M. Gilbert, B.T. Grenfell, S.A. Levin, T.P. Robinson, A. Teillant and R. Laxminarayan. 2015. Global trends in antimicrobial use in food animals. Proceedings of the National Academy of Sciences 112:5649-5654.

Wilson, C. 2020. Animal tuberculosis, Clinical Tuberculosis. CRC Press. pp. 415-435.

World Health Organization (WHO). 2021. Antimicrobial resistance: global report on surveillance. WHO Press.

Zheng, R., S. Xie, X. Lu, L. Sun, Y. Zhou, Y. Zhang and K. Wang. 2018. A systematic review and meta-analysis of epidemiology and clinical manifestations of human brucellosis in China. BioMed Research International 2018:5712920.

Zhou, X., Y. Wang, H. Liu, F. Guo, S.A. Doi, C. Smith and R.J. Soares Magalhães. 2018. Effectiveness of market-level biosecurity at reducing exposure of poultry and humans to avian influenza: a systematic review and meta-analysis. The Journal of Infectious Diseases 218:1861-1875.

Zinsstag, J., E. Schelling, D. Waltner-Toews and M. Tanner. 2011. From "one medicine" to "one health" and systemic approaches to health and well-being. Preventive veterinary medicine 101:148-156.